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Post-processing: Minimum Match 0%
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length: 2000000000
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FEATURES
                                       source
                                                   Unclassified.

1 (bases 1 to 1026)
Wayne, J. and Xu, S.
Method for construction of thermus E.
Method for construction of thermus plasmid
identification of two Thermus plasmid
patent: US 6207377-A 4 27-MAR-2001;
Location/Qualifiers
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Sequence 4 from patent US 6207377.
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AR139424.1 GI:14481920
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Identification of a thermophilic plasmid origin within a new Thermus-E. coli shuttle vector Gene 195 (2), 321-328 (1997)
97449309
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Thermus sp. YS45 replication
U89376
U89376.1 GI:2465516
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Direct Submission
Submitted (12-FEB-1997)
Road, Beverly, MA 01915,
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Thermus sp. YS45
Bacteria; Thermus/Deinococcus
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344. 1369
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/strain="YS45"
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rep_origin RBS	gene CDS	FEATURES SOURCE Gene RBS CDS		LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
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Wayne, J. and Xu,S. Y.
Method for construction of thermus-E.
Identification of two Thermus plasmid
Patent: US 6207377-A 6 27-MAR-2001;
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30S ribosomal protein S2; 50S ribosomal protein S16; 30S ribosomal protein S2; 50S ribosomal protein L19; cell division protein FtsH homolog; elongation factor Ts; ffh; ftsH; glnB; glnD; nitrogen regulatory protein pII; prophage; protein pII uridylyltransferase; pyrH; RNA polymerase sigma factor WhiG; rpbS; rpsB; rpsP; signal peptidase I; signal recognition particle protein; sip1; sip2; sip3; sip4; trmD; tRNA (guanine-N1)-methyltransferase; tsf; uridylate kinase; whiG. streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-JUN-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
3 (bases 1 to 38962)
Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill, J., Barrell, B.G. and Rajandream, M.A Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae; 1 (bases 1 to 38962)
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                                                                                                                                                                                                                IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 2E1 lies between 7A1 and 6A9 on the AseI-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                  jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in codons is given for each CDS. Usually the highest scoring matc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded
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                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.nih.go.jp/
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                                                                                                                      /strain="A3(2)"
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                                                                                                                                                                                                 Location/Qualifiers
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                                                                                   .166
  .01,
  glnB,
  nitrogen
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length

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protein

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repeat_region
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GLEGANTAEHTGI ELVAVIGG YERGELSE RESDLÜLLLHOEGEDEKAVALLADELWE VW
DLGI DILDHSVETPOOARKTAGODLKVHLGLLADARHLAGDLGLTASLRTAVLADWRNOA
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AEARRELDVE BOLLLATGRAVORLALOEGODOVAA ELGILDADALLROV EAARVI SY
AGDVTWREVGRVLRSRSVR PRLRAMMNGRNGGK PVA ERSPLAEGYVEQDOEGAVLARTA
RPERDPALPILAAAAAAAOAGLPLSRHAVRRLAATAR PLPTPWPA PEAREOLVTLLGSGR
PTVOVWEALEAEGLVTRLLEDWERVRCRPQRNAVHLWTVDRHLI ETAVRAAGETRRVH
RPDLLLI TAALLHDI GKOWPGDISVAGET I ARDVVAARIGFDGADTAVLATILV RHHLLLV
ETATRRDLDDPATVRAVAQAVGTEHTLELLHALTEADALATGPAAWSSWRGSLVADLV
KRVSGVLAGEPOPEAESAAPTAEGERLAVEAFRTGGDFVLALRAQTEP PAOSAPAPSSP
SSPSFPSPLSSPSSADGEPELGVELLI AVEDGAGVLPAVAGVLPAMHLLTVRTAEL
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GGHSPLLVACDLQRPNAVNQLSVVAERAGVAVVAPERGKGVDPVKVAKDSIEERAKK
VHDLVIVDTAGRIGIOGELMQQAADIRDAVSDEILFVVDAMIGODAVMTAEAFRDGV
FFDVUSKLDGDARGGAALSKASKKGQDETLDFVDAMIGODAVMTAEAFRDGV
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DLLTLLEQAEKTFSQEEAEKMASKJASKKGQDETLDFLAQMEQVRKMCSISKLIGMG
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DLLTLLEQAEKTFSQEEAEKMASKJASKKGQDETLDFLAGMEQVRKMCSISKLIGMC
DLGGMGQMKDQINNLDEBDYDRTAAIIKSMTPGERQEPTIINGSRRARIAKGSGVEVSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"SC2E1.03, ffh, signal recognition particle protein, len: 550 aa; highly similar to mmay e.g. SR84_ECOLI (453 aa), fatsa scores; opt: 1465 z-score: 1282.8 E(): 0, 50.0% identity in 458 aa overlap. Contains PS00017 ATP/GTP-binding site motif A (P-loop), PS00300 SRP54-type proteins GTP-binding domain signature and Pfam match to entry SRP54 PF00448, SRP54-type proteins, score 66.57. Similarities suggest possible start site at aa 35"
KNLVERFFEARKMMSRMAQGGGMPGMPGMPGMGGGPGRQKKQQKKAKGKQRSGNPMKF
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2719. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partial CDS, len: >54 aa; highly similar to many e.g. GLNB_AZOBR (112 aa), fasta scores; opt: 198 z-score: []: 4.9e-14, 50.0% identity in 54 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GI:3191979"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=]
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acctcgccctagacatggccaacggcgtgctctccttcaactgggtcaaggcctaccagg
                                                          CCGCGCTGCTGCACGACATCGGCCAAAGGCTGGCCCGGCGACCACTCCGTGGCCGGCGAGA 1662
                                                                                                                                                                      GCTGCCGCCCGCAGCGCAACGCCGTGCACCTGTGGACCGTGGACCGGCACCTGATCGAGA 1542
                                                                                                                                                                                                                                                                                                                             tcacccggcagaccgtccacgcctggaagaaggtccttgagaaaaagggcctggtggcca 493
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                                                                                                                                                                                                           ccgacgtccttcaccaaaccgtcaacggggagcgcggggccatcggcaccctttgggccg 553
                                                                                                           tccggctgaggccagggaaagccaggctcaccctggacgactacatctacccctggagga 613
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4504 .6450
/gene="ftsH"
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/protein_id="CaA19379.1"
/protein_id="CaA19379.1"
/protein_id="CaA19379.1"
/db_xref="Ci3191980"
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/db_xref="SPTREMBL:069875"
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LIVLIANLYLSFENEDDEPTISYTEFSKQVDEGNVSKIYAKGDA1QGQLKKARDNP-
EGDGTYTKFTTERPTFADDQLWADLTKNRVTVTAEPVVQHRSFLANLLIALAPMLILV
VLWIFIARNRGALGGGAGGMLGRKAPPKPVELEAGKPRTFFADVAGIDEVEGELSDV
VLWIFIARNRGALGGGAGGMLGRKAPPKPVELEAGKPRTFFADVAGIDEVEGELSDV
VDFLKNPDAYRRMGAKMPRGVLLTGPPGTGKTLLARANGGASGFTEMI
VGVGASRVRELFAEARKVAPSIFIDEDDTIGRARGGGSGTGGHDERGCTLNQILTEM
UGFSGSEGVIVIAATURADILDAALTRPGRFDRVVSVSPPDBGGREAILEHTREIPL
ADDTILAVURSTENDAMTGAFTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SC2E1.04, ftsH, cell division protein FtsH homolog (zinc metalloprotease, integral membrane protein), len: 648 aa; similar to many e.g. FTSH_LACLA (695 aa), fasta scores; opt: 1489 z-score: 1195.5 E(): 0, 41.7% identity in 640 aa overlap. Contains PS00017 ATP/GTP-binding site motif A (P-loop), PS00674 AAA-protein family signature and Pfam matches to entry AAA PF00004, ATPases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEEYLRGRIIGALGGMAAEHVVYGMITTGSESDLEQVTNIARGMVARWGMSERVGRLS
ALPGDAQQAYGLAAAPQTLDAIDGEMRRVVDSCYEEAVRKLRDHRGQLDALAESLLAS
ETLDEADAYRIAGITRLTKDDPEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 various cellular activities (AAA) and to entry zn-protease PF00099, Zinc-binding metalloprotease domain, score 22.07, score 357 96. Proline-rich N-terminus is not present in other ftsH homologs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry AAA PF00004, ATPases associated with various cellular activities (AAA), score 357.96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQQEQEEAARRAAAAQSGGALGLPQQGGQDFELPDEFKKFMG
3155. .3178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APDIDLAQVARTTPGMTGAELANLANEAALLAVKRKQERVTQANLSEALEKVQLGAER
PLVMPEEERRRTAYHESGHALLGMLQPGADPVRKITIVPRGRALGVTLSTPDADKYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
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4405. .445
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proteins, score 66.57"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ffh"
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Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Firminorto.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-MAY-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
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Streptomyces coelicolor
AL356992
                                                                                                                                                             The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at hit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces coelicolor A3(4)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
correct initiation codon. Where possible we choose an initiatic codon (atg, gratty or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the n
                                                                                jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strand)
                                                                                                                                              http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 13347)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 13347)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13347 bp
cosmid C42
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                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            small overlap between neighbouring submissions. Cosmid C42 Overlaps with cosmid C24 on the AseI-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    upstream initiation codon.

IMPORMANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                 complement(1254. .2285)
/gene="SC42.03c"
/gene="SC42.03c"
/note="SC42.03c, possible ABC-transporter ATP-binding
/notein, len: 343 aa; similar to SW:YRBF_HAEIN
/EMBL:U32788) Haemophilus influenzae hypothetical
ABC-transporter ATP-binding protein HI1087, 264 aa; fasta
scores: opt: 680 z-score: 686.6 E(): 8.9e-31; 41.48
identity in 244 aa overlap. Contains Pfam match to entry
PF00005 ABC_tran, ABC transporter and matches to Prosite
entries PS00017 ATP/GTP-binding site motif A (P-loop) and
PS00211 ABC transporters family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(493..1257)

/gene="SCC42.02c"
/gene="SCC42.02c"
/note="SCC42.02c, possible ABC-transporter integral
/note="SCC42.02c, possible ABC-transporter integral
membrane protein, len: 254 aa; similar to TR:053546
(EMBL:AL02002) Mycobacterium tuberculosis hypothetical
(EMBL:AL02002) Mycobacterium tuberculosis hypothetical
26.6 kD protein MTV023.08c, 254 aa; fasta scores: opt: 88
2-score: 1004.0 E(): 0; 55.8% identity in 242 aa overlap.
Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCC42.01c, possible ABC-transporter integral membrane protein (fragment), len: >161 aa; similar to TR:03545 (EMBL:AL022022) Mycobacterium tuberculosis hypothetical 29.6 kD protein MTV023.07c, 280 aa; fast scores; opt: 565 z-score: 630.0 E(): 1.3e-27; 54.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identity in 154 aa overlap. Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St8A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(491. .494) complement(493. .1257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="masplywldrsgdqllfyvrallwvprtlrrylkevqrllaeva
rgsgglgviggtigvmiamtlftgtvvgiqgvaaldqigtsaftgfvsayfntreiap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein (fragment)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<1.
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/strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MITGALROTGRLFALAAEVVRAVFRRPFQFREFVEQFWFVASVT
ILPAALVSIPFGAVIALQVGSLTEQLGAQSFTGGASVLAVVQQASPLIVALLIAGAGG
SAICADLGSRRIREELDAMEYMGVSEVQRLVVPRVLAAMGVAVLLNGLVSVVGILGGV
FENVLMQGGTPGAYLSSFSALAQLPDLYVSELKALVFGFIAGIVAAYRGLNPRGGPKG
VGDAVNQSVVITELLLFFVNNYMTAVVLQIVPPKGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB92894.1"
/db_xref="GI:8247036"
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                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative ABC-transporter integral membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVAGLALSATVGAGFTAQLGAMRINEEVDALEGMGIRSMPYLVTTRIIAGVVAIIPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ABC-transporter integral membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB92895.1"
/db_xref="GI:8247037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                      /gene="SCC42.03c"
      /transl_table=11
                                     /codon_start=1
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                                                                                                                                                                                                                                    /translatide=11
/product="putative secreted protein"
/prodin_1d="CaB92898.1"
/prodin_1d="CaB92898.1"
/protein_1d="CaB92898.1"
/protein_1d="CaB92898.1"
/db_xref="01:8247040"
/db_xref="01:8247040"
/translation="MKATPANAPRPSRARARTTSIAAFVVLAALVPTTASASGTQEVE
AELPYVCTLESGQLPATVRVSAEPERRAGADEAFTPSDYTTVELPAEAVADLTARDA
AEVRARTSLAVGVAQNTATAAVTWRGSAEPVALPGSGPLTLVTRGDVBPSVAGRSDGDL
TFSAGALAIDLALGAADPATADPGSLTVDCTLAEDAPGGGLLATVPVGTDGQAPSGSP
SSGGPAGSSGAPDDDGCRQDGPGDRREPERQSERSPKVLENTPGANADDDVPPCRKDEQ
PSTDVSLNAVVTGYANVKMKGAAYLPPSCVLIEQGLPVPGPPDDEYLIPDTLSYAN
FHYRERKQTPPFEATFLSSEDFAPVKATMVLEQTGTMRIDSRMKIRLSDETTITDTYVR
APLVLHVLDLEVNGTPLDVGSECRTETSLTSEDPDAMFPGDHLVLYGRGEQLIGLPA
TGYLLLSGGALSGEATIPAFTGCGSDEDLDRLITASVSGPGNYIKQVQGQTCAIAAP
VFPSDENEGQCTEDLQPYEIFVAER"
5323..6264
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/gene="SCC42.03c"
/note="PS00211 ABC transporters facomplement(2133...2156)
/gene="SCC42.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCC42.03.
/note="PS00017 /
2904. .2909
                                                           sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCC42.05"
3687. .5288
/gene="SCC42.05"
/note="SCC42.05"
/note="SCC42.05, possible secreted protein, len: 53
Contains possible N-terminal region signal peptide
sequence. High content in alanine amino acid residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3679. .
3687. .
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avnvgnivltatipmtcttstaagtmasatgnpgdvadittmnpgasgspctsvlgnv
tttsvtpwdvvgvdynsstgvtkgyvgnvkanvtagackftvtgkasgtytnstgvla
instagelavsnpvncgaivttatkptfkgnvavtvastgaiptivgsnp"
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/protein_id="CAB92896.1"
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/db_xref="GI:847038"
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PSGTGKTVFLKSLIGLLKPEKGGVLINGVDMVNSPERDIYETRKLFGLMFQDGALFGS
MSLFDNIAFPLREHTRKKESEIRRIVMERIEVVFLLGAGKLPGEISGGMKRAGGLAG
ALVLDPQIILCDEPDSGLDPVRTAYISGLLDLNAQLDATMLIVTHNLDIAATVPDNM
ALVLDPQIILCDEPDSGLDPVRTAYISGLEDLIDLNAQLDATMLTVTHNLDIAATVPDNM
GMLFLRGLVTFGPREVLLTSSDEPVVAGFLGGRREGPTGMSEEKDAATLAAEADAAPAA
/product="putative secreted
                            /codon_start=1
/transl_table=11
                                                                                                                                  /gene="SCC42.06"
/note="SCC42.06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative secreted /protein_id="CAB92897.1" /db_xref="GI:8247039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCC42.04"
/note="SCC42.04, p
Contains possible
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2918. .3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1620. .2177)
/gene="SCC42.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=]
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complement/1777
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                                                                                                                                                                                                        .6264
."SCC42.06"
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                                                                                                                                  possible
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                                                                                                  N-terminal region signal |
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5.4e-42"
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                                                                                                                            313 aa
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ORGANISM
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SC2D46
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgtgctggtcctctgggctcaggggaaaaggggtgatgcccaacaccaagaccgtggccgt 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGCTGTGGGTCCCGCGGACCCTGCGCCGCCTACCTCAAGGAGGTGCAGCGCCTCCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gctcaccctggacgactacatctacccctggaggaacctcgccctagacatggccaacgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATGGTGATGACGGCCGTCTACCTCCAGATCGTCCCGCCGAAGGGAGGCTGAGGTCCGAT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgtgctctccttcaactgggtcaaggcctaccaggaccacggaatccgccccaccctgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCTCCCCGCTCGGCTCGACCGCCTCCGGCGACCAACTGCTCTTCTACGTCCGGGC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c9999agcgccgggccatcggcaccctttgggccgtccggctgaggccagggaaagccag 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTCGGCGACGCCGTCAACCAGTCCGTCGTCATCACCTTCCTCCTGCTCTTCGTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcaccaaaccgtcaa 518
                                                                                                                                                                                                                                                                                                                                                                                                                                    AL391406.1 GI:9857143
AbaA-like; AraC-family; ATP/GTP-binding membrane; bldA;
AbaA-like; AraC-family transcriptional regulator; hydrolase;
integral; integrase; MarR-family; NLP/P60-family secreted; pgm
phosphoglycerate mutase; TetR-family; transferase; transport.
Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Fitmicutes; Actinobacteria; Actinobacteridae;
Notes:
Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                  Submitted (03-AUG-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                             3 (bases 1 to 35576)
Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                  2 (bases 1 to 35576)
Brown, S.P. and Harris, D.
                                                                                Colney, Norwich, Norfolk NR4
                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                             Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                  Actinomycetales; Streptomycineae; Strepto
1 (bases 1 to 35576)
Redenbach, M., Kleser, H.M., Denapaite, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SC2D46
Streptomyces coelicolor
AL391406
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45.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35576 bp DNA cosmid 2D46.
                                                                                  7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                Actinobacteridae; antomycetaceae; Streptomyces.
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FEATURES
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The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 2D46 lies between and overlaps cosmids D66 and D8 on the AseI-D genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SCTB7.01c. SC (S.coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       more significant matches with motifs in the PROSITE database
/note="2SCD46.02, possible GntR-family transcriptional regulator, len: 303aa; similar to many eg. TR:Q9RIQ2 (EMBL:AJ243257) KORA protein from plasmid pSNA1 of Streptomyces natalensis (245 aa) fasta scores; opt: 175, z-score: 204.2, E(): 0.00069, 28.2% identity in 238 aa overlap. Also strongly similar to neighbouring CDS 2SCD46.04 fasta scores; opt: 1074, z-score: 984.2, E(): 0, 57.6% identity in 302 aa overlap. Contains Pfam match to entry PF00392 gntR, Bacterial regulatory proteins, gntR family and helix-turn-helix motif (Score 1967 (+5.89 SD))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="25CD46.01c"
/note="25CD46.01c, unknown, partial CDS, len: >45aa;
/note="25CD46.01c, unknown, partial CDS, len: >45aa;
strongly similar to neighbouring CDS 25CD46.03c fasta
scores; opt: 169, z-score: 236.7, E(): 1.4e-07, 51.1%
identity in 45 aa overlap. Hydrophobic."
                                                                                                                                                                                                                                                                                                                                                                                                              /gene="2SCD46.02"
289. .1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(142. .147)
289. .1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Nominal overlap with Streptomyces coelicolor cosmid
D66 (EMBL:AL358692)"
                                                                                                                                                                                                                                                                                                                                   /gene="2SCD46.02"
/note="2SCD46.02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="CACO4023.1"
/db_xref="GI:9857144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Repeated degenerately at 1210...2414. This DNA repeat manifests as a duplication of a pairs of CDSs such that 2SCD46.01c is similar to 2SCD46.03c and 2SCD46.02 is similar to 2SCD46.04."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MPLIAIVVAALAIGFEQLVQWKYGPMGIIAFVALSIGIKAKNTMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="cosmid 2D46"
complement(1. .135)
/gene="2SCD46.01c"
1. .1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D66 and D8 on the
                                                                  gene
   CDS
                                                                                                                                                                                                                                          misc_feature
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/note="2SCD46.04, possible GntR-family transcriptional regulator, len: 291aa; similar to many eg. TR:09RIQ2 (EMBL:AJ424257) KorA protein from plasmid pSNA1 of Streptomyces natalensis (245 aa) fasta scores; opt: 175, z-score: 209.9, E(): 0.00033, 29.9% identity in 194 aa overlap. Also strongly similar to neighbouring CDS 2SCD46.02 fasta scores; opt: 1074, z-score: 984.2, E(): 0, 57.6% identity in 302 aa overlap. Contains Pfam match to entry pPG0392 gptR. Bacterial regulatory proteins, gntR family and helix-turn-helix motif (Score 2173 (+6.59 SD)) at residue 41-62. Note possible alternative downstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="2SCD46.04"
1539. .2414
/gene="2SCD46.05"
2363, 3104
                                                                                 regulatory proteins, 7.2e-20"
                                                                                                                                                                                                                                                                                                                 /translation="MVVTQENVSVNGSRRLSSQEIADVLRERIRGGDLRAGDRLPTQA
ELAEEFGVERGTVRQALRALQEDGLLTNVSKGSPPRIAEPATPRAEPQPTMVALGPRL
AEAFAAPHVRVDVVCHTSETLMLALSEPLRLTHEGRIHPESIDFRVLMPSRDIALAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Repeated degenerately at 1210. .2414. This DNA repeat manifests as a duplication of a pairs of CDSs such that 25CD46.01c is similar to 25CD46.03c and 25CD46.02 is similar to 25CD46.03c."
                                                                                                                                                                                                                                                       LNGEEALLGYYMLTRREEEYESRTLQMYDALGSQSLLFSFLNRTGHRDAVFVEESQKW
                                                                                                                                                                                                                                                                                              VLVEDEEDDPVHQRWLQMRNAQARVLQHNLHAVRSTHRVDVRIAFRALPFTPPMKLYI
                                                                                                                                                                                                                                                                                                                                                                                                                         /trans_table=11
/product="putative GntR-family transcriptional regulator"
/protein_id="CaCO4026.1"
/db_xref="GI:9857147"
                                                                                                                                                     /note="Pfam match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translational start codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1210...1398)

/gene="25CD46.03c"
/gene="25CD46.03c"
/note="25CD46.03c, unknown, len: 62aa; strongly simila neighbouring CDS 25CD46.03c fasta scores; opt: 169, z-score: 236.7, E(): 1.4e-07, 51.1% identity in 45 aa overlap. Hydrophobic."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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/note="2SCD46.04,
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/protein_id="CAC04025.1"
/db_xref="GI:987146"
/translation="MPVLALVSAVFVIAFEQIVQWRYGATGIVGLLLLTIGIKAKSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative GntR-family transcriptional regulator"
/protein_id="CACO4024.1"
/db_xref="GI:9857145"
/translation="MYVEPEHAPVNGRERPQRPQATHREVADELRARIRSGRLRPGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1210.
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PSGDIDLAFPVAVSGGAAGGPVHERWLAMRNAQGQVLRHNLLSLRATHGIDVRVSFRA
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                                                                                                              gntR family, score 69.30, E-value
                                                                                                                                           entry PF00392 gntR, Bacterial
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ACCESSION
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Best Local S
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     ORGANÍSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggtcaaggcctaccaggaccacggaatccgccccaccctggacgtgctggtcctctggg 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acatotaccoctggaggaacctogcoctagacatggccaacggcgtgctctccttcaact 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tcggcaccctttgggccgtccggctgaggccagggaaagccaggctcacccttggacgact 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTCACCCGGCCACCACCGCCCTCCCGCCCGTCGAACTGGCCCCCGGCGTCC 16427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaaagggcctggtggccaccgacgtccttcaccaaaccgtcaacggggagcgccgggcca 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAACGTCTACATCGTGGAGCTGGCGCAGCGCCTCGCCGCGATCAACATCGAGGTCGAGA 16367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGGGGGGGGCGCCCTGGTGCACGCCATGCACCATGGCCAAGGTCAAGAACGCCAACC 16667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctcaggggaaaagggtgatgccaacaccaagaccgtggccgttgacctgggcctcatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTCTGCGCCTTCACCCACGGCGTGATGCAGGCCTGGGCCGGTCACCGCCCCGGCCACT 16547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCCGACGGCGA 16680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tggtcctccccga 788
Arp-dependent RNA helicase; DNA polymerase III submit gamma; ARP-dependent RNA helicase; DNA polymerase III submit gamma; DNA-binding protein; integral membrane protein; lipoprotein; LSR2-like protein; luxx family; phosphoribosyl formylglycinamidine synthase II; phosphoribosylaminoimidazole-succinocarboxamide synthase; phosphoribosylformylglycinamidine cyclo-ligase; phosphoribosylformylglycinamidine cyclo-ligase; phosphoribosylformylglycinamidine synthase I; secreted peptidase; phosphoribosylformylglycinamidine synthase I; secreted peptidase; sensor kinase; transposase; trNA; two-component transcriptional regulator; valine dehydrogenase.
Streptomyces coelicolor A3(2).
                                                                                                                                                                                                                                                                                   Streptomyces coelicolor cosmid D25.
AL118514
AL118514.1 GI:5918466
ABC transport protein, ATP-binding subunit;
amidophosphoribosyltransferase; ATP-dependent helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/note="2SCD46.05, possible hydrolase, len: 273aa; weakly similar to many proposed phosphatases eg. TR:CAB84916 (EMBL:AL162756) putative phosphatase from Neisseria meningitidis (235 aa) fasta scores; opt: 195, z-score: 238.2, E(): 8.8e-06, 29.5% identity in 237 aa overlap. Contains pfam match to entry PR00702 Hydrolase, haloacid dehalogenase-like hydrolase. Note possible alternative downstream translational start codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"putative hydrolase"
/protesin_id="CAc04027.1"
/protesin_id="CAc04027.1"
/db_xref-"gi:9857148"
/translation="MVRRPLGNHHHGHDTLLVTSDTDOTEPVSERTGRDEQSEALRDL
/translation="MVRRPLGNHHGHDTLLVTSDTDOTEPVSERTGRDEQVHPDPHVLL
/translation="MVRRPLGNHHGHDTLLVDWLERLGLKELLTQEEQVHPDPHVLL
/VGARVVLWDFDGFICRLFAGYSADRVAGELVDWLERLGCKELLTQEEQVHPDHVLL
AAVDRRHRRSDLVAEFEERLTREELRAVPTAMPTAYADALIRTWSALGVGLAVTINUS
ARVSEYLETROLLGCFARHIYGRTGDPHLLKPDPHCLNRALSAMGAAPARALMVGDS
RRVVSEYLETROLLGCFARHIYGRTGDPHLLKPDPHCLNRALSAMGAAPARALMVGDS
ASDVTAARRAGVPFLGYGHNERKTKLLKQAGADTVVDSLEPVLRLLWENGTPAPA"
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/transl_table=11
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46.6%;
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Pred. No. 1
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The length in codons is given for each CDS.

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The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given the position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nib.or.in/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted (20-SEP-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kedennach, A. And Hopwood, D.A.
Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
and Microbiol. 21(1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by the BBSRC and Beowulf Genomics

Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jun/cgi bin/frameplott.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon. If this cannot be identified we choose the mesure the initiation codon. If the cannot be identified we choose the most upstream initiation codon. Or be the entire insert of the importance in the initiation codon. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlaps between neighbouring submissions.

Cosmid D25 Overlaps with cosmid D17 on the AseI-D genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomson, N.R.,
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                                                                                                                                                                                      /note-"SCD23.01c, possible transposase, partial CDS, len: > 150 aa. Similar to many e.g. Methylobacterium sp TR:Q50409 (EMBL; X96995) transposase IS1357 (411 aa), fasta scores opt: 239 z-score: 312.5 E(): 4.7e-10 38.2% identity in 131 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCD25.01c"
complemen+//
                                                                                                                                                                                                                                                                                                                                                                                 complement(<1...451)
/gene="SCD25.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:100226"
/clone="cosmid D25"
/product="putative transposase"
/protein_id="CAB56345.1"
/db_xref="GI:5918467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor A3(2)"
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gene

CDS

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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                (phosphoribosylglycinamide synthetase) MTCY369.17 (422 aa), fasta scores opt: 957 z-score: 1033.0 E(): 0 58.3% identity in 424 aa overlap. Contains a PS00184 Phosphoribosylglycinamide synthetase signature and a Pfam match to entry PP01071 GARS, Phosphoribosylglycinamide
                                                                                                                   /gene="purb"
/gene="SCD25.04, phosphoribosylamine-glycine ligase (EC 6.3.4.13), len: 416 aa. Highly similar to many e.g.
Mycobacterium tuberculosis SW:PUR2_MYCTU (EMBL; Z:80226)
phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS)
(glycinamide ribonucleotide synthetase)
                                                                                                                                                                                                                                                                                                                                4300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="dnaz"
/note="5.03, DNA polymerase III subunit gamma, len:
784 aa. Highly similar to the gamma subunit of
Mycobacterium tuberculosis SW:DP3X_MYCTU (EMBL; AL022121)
(EC 2.7.7.7) DNA polymerase III subunit gamma/tau (578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           database similarities. Contains site motif A (P-loop)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identity in 435 aa overlap. Note that after residue 433 the C-terminus of this protein has no significant database similarities. Contains a PS00017 ATP/GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="tRNA Ser anticodon GGA, Cove score 72.31"
/product="tRNA-Ser"
1826. _4180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRYGLEAEAEVALANRRSVSDAVVTGPNGLRIGREIQYHHLSPSSVRRRSVNALEHGV
TPLWVAKDRTASLIDRAPWARVDDMPWKDIADGKEMVIRGGYRHLEVWKCVPSSERHC
                                                                                                                                                                                                                                                                             /gene="purD"
4300. .5550
                                                                                                                                                                                                                                                                                                                                                     /gene="dnaz"
/note="PS00017
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1826. .4180
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PVRGLDQSTGGFTLPHARQALSRPDANHHCGTCRRLRRAGLSAVGAGPSSTGASRKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein SCD25.02"
/protein_id="CAB56346.1"
/db_xref="G1:5918468"
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/note="SCD25.02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MFIRRGRVGGRRPLVASHLPITHKATPAESAQHKATKERIVEAA/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.7.7.7) DNA polymerase III subunit gamma/tau (fasta scores opt: 1757 z-score: 1081.7 E(): 0
                                                                                                                                                                                                                                                                                                                                .5550
                                                                                                                                                                                                                                                                                                                                               ATP/GTP-binding site motif A (P-loop)."
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CTCCCGCAAGGGCCGCACCATCATCTTCGTCCGCACCCAGCTGG 39727
                                                                              GTCGCACCACATCCTGGTCGTGAAGCCCAAGGACAAGGCGCCGGTCACCGCGGCCATCGC
                                                                                                         caccctggacgtgctggtcctctgggctcaggggaaaagggtgatgcccaacaccaagac 749
                                                                                                                                                          GTACCTGAAGGACCCGGCCTCCACGAGGTCGACGCCCCAGGGTGCCGTGACGACCAT
                                                                                                                                                                                                                                        CGGCCAGCGGATGCTGTTCTCCGCCACCATGGAGAACGAGATCAAGACCCTCGTCGACCG 39563
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                                 cgtggccgttgacctgggcctcatcctggtcctccccgaggtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="SCD25.05, possible integral membrane protein, 664 aa. Contains a degenerate direct repeat region: residues 469_ PNADDEA P HAPYADDEA L HYPDADDEA P HAPYAD_502. Also contains possible membrane spanning hydrophobic domains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCD25.05"
5857. .7851
/gene="SCD25.05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mkvlvigggarehalcrslsldpdvtalhcapgnagiaevaelh
Qvdaldgaavtalagrlgaelvvvgpeaplvagvadavreagipvfgpsgeaarlegs
Kafakdymacagvptarsyvctnpaevdaalaafgapyvvkddglaagkgvvvtddve
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5857. .78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative integral membrane
/protein_id="CAB56349.1"
/db_xref="GI:5918471"
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/db_xref="GI:5918470"
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45.8%;
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Best Local Similarity

Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                 cccctggaggaacctcgccctagacatggccaacggcgtgctctccttcaactgggtcaa 662
  GGGCGAGGTG 88765
                                        ccccgaggtg
                                                                                     CAAGCAGCAGATCGCCAAGAACTCCACCCACGACGACGACCACCACCACCACCACCTCGTCCTCCA 88755
                                                                                                                         gaaaagggtgatgcccaacaccaagaccgtggccgttgacctgggcctcatcctggtcct 782
                                                                                                                                                                        GACCGTCCACGGCAACAAGTTCAGGTTCCGCGTCGAGCCCGGCCGCACCGTCGGCTACGT 88695
                                                                                                                                                                                                ggcctaccaggaccacggaatccgcccaccctggacgtgctggtcctctgggctcaggg 722
                                                                                                                                                                                                                                                             CCACGGCAACGTCCTCCACCTCGTCATCCGCATCTCCGACCTCCGCCTCATCACCGTCCA
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PROGRESS ***, 2 ordered p
AC105260
AC105260.1 GI:17985870
HTG; HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (28-DEC-2001) Institute of Botany, Academia Sinica, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan The nucleotide sequence of this BAC clone was generated by combining Monsanto and ASPGC-Taiwan sequencing data.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces are represented as runs of N. The order of the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chow,T.-Y., Hsing,Y.-i.C., Chen,C.-S., Chen,H.-H., Wu,H.-P., Liu,S.-M., Chao,Y.-T., Chang,S.-J., Chen,T.-R., Chen,Y.-L., Chow,M.-H.J., Hong,Y.-C., Hsiung,J.-N., Hsu,C.-H., Huang,J.-J., Kau,P.-I., Lee,M.-C., Leu,H.-L., Lin,S.-J., Wu,L.-F. and Shaw,J.-F. Oryza sativa BAC OJ1115D04 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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1 39588: contig of 39588 bp in length 39589 39608: gap of unknown length 39609 100772: contig of 61164 bp in length.
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ow,T.-Y. and Hsing,Y.-I.C.
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illarity 50.8%;
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/db_xref="taxon:4530"
/chromosome="5"
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gggctcaggggaaaagggtgatgcccaacaccaagaccgtggccgttgacctgggcctca 772
                                                                                      CCACCAACGGCGACACCCACCTCGGCGGCGAGGACTTCGACCAACGCCTCATGGACCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced
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Ehrhartoideae; Oryzeae; Oryzeae;
1 (bases 1 to 167049)
Sasakl,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa chromosome PROGRESS ***, in ordered
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A set of ordered cosmids and a detailed genetic and physical map
for the 8 Mb Streptomyces coelicolor A3(2) chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC8A2
Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor sequencing at The Sanger Centre is funded
by the BBSRC and Beowulf Genomics
by the Coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof
David A. Hopwood, [3] John Innes Centre, Norwich Research Park
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-OCT-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor A3(2). Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                   http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Notes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                             IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for
                                                                                                                 restriction fragment.
                                                                                                                                                                                                                                                                               upstream initiation codon
                                                                                                                                      petween and overlaps cosmids 4A7
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                                                                                                                                           overlap between neighbouring submissions. en and overlaps cosmids 4A7 and C42 on the
/organism="Streptomyces
/strain="A3(2)"
                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to 7459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Harris, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7459 bp
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                             coelicolor A3(2)"
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                                                                                                                                        the AseI-C genomic
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                                                                                                                                                                                                                                                                                                               choose the most
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                                                                                                                                                                      8A2 Lies
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        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative secreted protein"
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/protein_id="CAC12793.1"
/db_xref="GI:10798657"
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/translation="MITLAVRLKNLAFILIAVLALSFLGIRYADLGRYVGVADYYTVD
/translation="MITLAVRLKNLAFILIAVLALSFLGIRYADLGRYVGVADYYTVD
/translation="MITLAVRLKNLAFILIAVLARSFLERIKKAPRIFADTRAVVAG
LYNAGEOYIDLRPESDGSPYLADGTRIEQADTRAFILINDGETVLRTQAQEARA
TRANGEOYIDLRPESDGSPYLADGTRIEQADTRALPSTTLLINDGETVLRTQAQEARA
TRANGEOXIGHAAAALKGSDADLRRLLAVTPEAATQVSGLLRDLDPSLGVYLANLLTT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="cosmid 8A2"
complement(1. .126)
/gene="SC8A2.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVAVTRORGIEELLVKYPAAVSAGATAVDGGKLDLGLAVTFFSPLPCTDGYGGTRYRNGLDLGTAPALNTDAACTAPASGGKNVRGSANAPKSGAVPDPATPGSLPSGGGRTTPAGGGSPARDGSTALPGALALPGOSGEAPAGLTGLLAPAAGGAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis hypothetical 46.7 kDa protein MTV051.09, aa; fasta scores: opt: 529 z-score: 488.9 E(): 1e-19; 31.3% identity in 438 aa overlap. Contains Pfam match entry PF02470 mce. Also contains possible N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SC8A2.02c, possible secreted protein, len: similar to TR:053972 (EMBL:AL022073) Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="SC8A2.03c, possible secreted protein, len: 413 aa; similar to TR:053971 (EMBL:ALO22073) Mycobacterium tuberculosis hypothetical 40.2 kDa protein MTV051.08, 377 aa; fasta scores: opt: 685 z-score: 681.0 E(): 2.le-30; 36.0% identity in 311 aa overlap. Contains Fam match to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region signal pe
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC8A2.02c"
/note="scax
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complement/"~~
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                                                                                                                                                                                                DLPLPGGADLGDHPYTVTAELQDVLSLVPHSAVRVNDVAVGRITGIELGEDDWSARVT
MEINGEVRLPADATARLEQSSLLGEKYVQLVAPAKETGTGRLTDGSVIPLARTSRNTE
VEEVFGALSLLLNGGGVNQLKTITRELNAALGGREPEVRSMLKRVNTLVGDLDDHRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry PF02470 mce.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1421. .../gene="SC8A2.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF02470 mce, , E-value 1.8e-25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="mrrarilagaglyLALgyCGTGAWTYTQARTDDGLAYGRERD"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
/product="putative secreted
/protein_id="CAC12792.1"
/db_xref="GI:10798656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          en:
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           /gene="SC8A2.03c"
                                                                                                                    YLSMVAVPGTEVIPPLVDGDTPGPTASATAQDGPDPAAKNPAAKNPISRKRSSGQRGS
                                                                                                                                              STINASKDDMIADLKAVAPTLRALADAGTDLPDSLQVLLTYPFTDEVLRGVKGDYLNT
                                                                                                                                                                                                                                                                                    /product="putative secreted protein"
/protein_id="CAC12794.1"
/db_xref="G1:10798658"
/translation="MKRATLPRGRVAGLTAGSLAAVGLALALTLGGVSVVPSGFDGIE
                                                                                                                                                                                                                                                                                                                                                                                                                             region signal
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC8A2.03c"
/note="scane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC8A2.02c"
                                                                                       ASPLPLPSVSGAGPASGGEHG'
                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                         [TDALDAVNRLSSTLATRKDDVGTVLTDLSPGLKTLERQRGSLLTMLRSLDTLSGVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="SC8A2.01c, possible secreted protein (fragment),
>42 aa. Contains possible N-terminal region signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Also contains possible N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score 98.10,
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Best Local
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34.6 atcocctacggcaaccgggagctctggaggaaggttggggacggtcgtcttcatggtcccc
                                                                               286 gccgtccaggacgggcctcagaagcttctggaactcctccaggagattgcccgctccacc 345
                                                                                                                                                      Local Similarity
                                                         GACGACCTGGCGAGCTCCGTGCCGCTGGAGGACCTGCGCACGGTCGTCGACGAGTTCGGC
                                                                                                                                       237;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3669: .4724)
/gene="SC8A2.05c"
/note="SC8A2.05c, possible secreted protein, len: 351 aa;
similar to TR:053969 (EMBL:AL022073) Mycobacterium
tuberculosis hypothetical 43.7 kDa protein MTV051.06, 410
aa; fasta scores: opt: 683 z-score: 769.5 E(): 0; 33.4%
identity in 368 aa overlap. Contains Pfam match to entry
PF02470 mce. Also contains possible N-terminal region
                                                                                                                                                                                                      complement(4721.
/gene="SC8A2.06c"
                                                                                                                                                                                                                                         E-value 6.7e-30"
                                                                                                                                                                                                                                                                                                                                                                                 RLAESFETLIEDGGPLLGELRDRRTAINALLKGSQDLGTELGGLVKDNEKQLGPTLKALG
                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTTYSADFSESAGLDEGDEVRIAGVKVGQVTGVALDGAKVKVSFEVEDAWIGDRTT
AAIAIKTVLGDKYLALDPLGSGRQDPGARIPLARTTSPYDVTQAFQDLSGTVDDIDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative secreted protein"
/protein_id="CAC12796.1"
/db_xref="G1:10798660"
/translation="MKRPRGKPLFKPVKERNPVAVGVAGLLVLTLVALLVYNVDRLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3669. .4724)
/gene="SC8A2.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2667. .2671)
/gene="SC8A2.04c"
complement(3238. .3654)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:10798659"
/tanaslatlon="MTBRRKILTGVLALVVLAAGGLAAARALGPGGTRVTAYFDRAIG
/translatlon="MTBRRKILTGVLALVVLAAGGLAAARALGPGGTRVTAYFDRAIG
/YAGSDLRILGVRVGEVESVDÞEGTRVRVGLRLDGIKVPEDAARAVVVAAFSVVAADRYV
QLTPAXRTGPALADGAVLPASRNHVPVEIDQIYDSITELGDALGPDGAAADGALSELL
RTGADNLDGNGEAIGDGVEQFGKAAKTLDGSSGDLFETLSSLQTFTTMLKNKDTDVRT
AQERLDEVVSFFADNKDDLTGALEELGKALGQVKTFIEDNRGELKKNVDRLVPITRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis hypothetical 44.4 kDa protein MTV051.07, 42: aa; fasta scores: opt: 596 z-score: 625.4 E(): 2.6e-27; 33.1% identity in 320 aa overlap. Contains Pfam match to entry PF02470 mee. Also contains possible N-terminal region signal peptide sequence"
                                                                                                                                                                                                                                                                             complement(4254. .4670)
/gene="SC8A2.05c"
                                                                                                                                                                                                                                                                                                                                                 RVTSVLEKNNTRLGETLALVGPYYRLVGNTLGNGRWFDSYLCGVVPRDYLPETSOPST
GCLPPKQPAAAQGSGAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SC8A2.04c, possible secreted protein, len:
similar to TR:053970 (EMBL:AL022073) Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SC8A2.04c"
/note="bf--
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/note="scoa
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E-value 8.5e-32"
                                                                                                                                                                                                                                                        /note="Pfam match to entry PF02470 mce,
                                                                                                                                                                                                                                                                                                                /gene="SC8A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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E-value 3.6e-27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEQRASLAEALDVAPLAADNVVNAYNPDTRTLDGRANLNEISSGGPLLPLPVAGTEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative secreted protein"
/protein_id="CAC12795.1"
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                                                                                                                                                  5.1%;
46.7%;
                                                                                                                                                                                                                                                                                                        7.05c"
                                                                                                                                Score 52.6; DB Pred. No. 5.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.04c"
                                                                                                                                 0,
                                                                                                                                                                 DB 1;
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                                                                                                                                 264;
                                                                                                                                                                 Length 7459;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                          score 112.80,
                                                                                                                                6,
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                                                                                                                                Gaps
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MEDLINE
REFERENCE
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                                                                                                           COMMENT
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ORGANISM
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                                                                                                           Notes:
                                                                                                                                                                                                                     Direct Submission
                    (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
 are numbered using the following system eg SC7B7.01c.
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AAGCTGGACCTCGGCCTGGCCGTCACC
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by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre
available on the World Wide Web.
                                                                                                                                                                                       Submitted (30-NOV-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA B-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 34983) Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                          Colney, Norwich, Norfolk NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase/reductase; glucose-1-phosphate adenylyltransferase; glycosyl transferase; hydrolase; integral membrane protein; lact-family transcriptional regulator; lysR-family transcriptional regulator; oxidoreductase; reductase; secreted protein; regulator; oxidoreductase; reductase; secreted protein; solute-binding protein; transport system permease protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34983 bp
Streptomyces coelicolor cosmid M
AL133278
                                                                                             Streptomyces coelicolor sequencing at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 34983)
Redenbach, M., Kieser, H.M., Denapaite, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acetyltransferase; alpha-mannosidase; dehydratase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transposase remnant.
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                                                                                                The Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eichner, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequenced clone. It may be overlapping sections once, small overlap between neigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            upstream initiation codon.
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http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overlap between neighbouring submissions.
/note="SCM11.02, possible integral membrane protein, len: 470 aa; similar to TR:P96418 (EMBL:292669) Mycobacterium tuberculosis hypothetical 54.8 kb (EMBL:29169) Mycobacterium TCV08D5.31c, 482 aa; fasta scores: opt: 2112 z-score: 2527.5 E(): 0; 61.9% identity in 472 aa overlap and to TR:069633 (EMBL:AL022121) Mycobacterium tuberculosis putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAHEVFDLRPEEYDGRPESLALRVPTAESRRMDTIVARAMKDGSENYGTYFRLRRRDG
TLRWTHTQGYLRRDETGRPRRIIGIVEDATQEMADLASREQAALDEARRRLTNVVQL
ATAALAHARTVDDVLDVLRDTHGLTRLGATSLVMGLVEAGRIRLVADGPENSFIPGRF
VTRIDEPYPMSEAVRTLSPRFIESPEEFAERYEGLWKDITHLDITAAAYLPLIAQARP
IGAIGLLYSDRHGFSPEDRNVLVALGSGIAQSLQRAMLYEQEMDLAEGLQQAMLPRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SCM11.01c, hypothetical protein, len: >587 aa; similar to various hypothetical proteins, e.g. TR:092BJ0 (EMBL.AL035161) Streptomyces coelicolor conserved hypothetical protein SC9C7.20, 860 aa; fasta scores: opt: 588 z-score: 654.5 E(): 4.4e-29; 30.4% identity in 542 aa
                                                                                                                                                                                                                                                                    /gene="SCM11.02"
1887. .3299
                                                                                                                                                                                                                                                                                                                                         /gene="SCM11.01c"
1874. .1879
1887. .3299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRVQQHVSPGDPEGLTEARHMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSVPGCDVAVRYRAASIGGALGRDIGGDWYDLIPLPGGRVĞAVIGDVQGHDTHAAAVM
GQLRIVLRAYAAEGHPPATVMARASVFLHELDTDRFATCLYAEADLGTGVVQVVRAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein SCM11.01c"
/protein_id="CAB61912.1"
/db_xref="G1:6522831"
/translation="MSDRGASAPSLPDDWPAHPDPILALNRMGSFDWDLDAGLFHMDA
                                                                                                                                                     /gene="SCM11.02"
/note="SCM11.02, po
470 aa; similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {	t GADLDEGMDVLTALITSGPQDVRDLADRLIDVVDERRGDDDVALLVLRRHGLGAPRTF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1. .1764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDPLLRFGDGTCRLVRVEGGLPLGLSAEFGRLAYPVATLELDPGNTLLLCTDGLVEQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:100226"
/clone="cosmid M11"
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/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="nominal overlap with Streptomyces colicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "SCM11.01c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coelicolor A3(2)"
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gene

FNGTAQRHGRTSVPSEHHAAYLIELSKAWADDPHRPVWLQEVGAPAPLVPAEHAAAFT

SAQIDAWLERMLAACEEGAPGRMHLHAEYDATWYQDDQPFTPAQAARQGAVTAVHSWV

RAARDGARPAPATTALAVPADPAARSACAPGGAVFDAFFRLVADGARPTTVLDTR*t*

CDS

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/translatation="MHDDRSLVEARILKRVLDERVRPALLYPESVPLDVAVWNAPGEPVP
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GEGLYYRPDGTPVKGLNPRNOWYRIGAPVEGEVALGELWAELPVSPFRWEILAVVD
CEGLYYRPDGTTEWDLAVLDETVWNLVLDLEVLGELMAELPVSPFRWEILAVVD
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KVARTTSNWTALLEDEPDFVFAMSQAQQWAWWRDHREFVWARVYKAVANDGRFVPAAGK
KVARTTSNWTALLEDEPDFVFAMSQAQQWAWWRDHREFVWARVKAVANDGRFVPAAGK
WYESDTNWFGSEAMARQFYHGKRFFLDEFGVENDEMLPDTFGFAAGLPQIIKAAGAK
YLLTQKISWSQTNKFPHHTFRWGIDGTRIFTHEPPVDTYNCSWKGSEIAHAATNFKD
KGVARHSLAPTGWGDGGGGTTREWNAKAARARLRNLEGSATVEWETPHAFFEKAEAENPA
PPVWVGELYLELHRATLTSQAKTKQGNRRSEHLLREAELWGIIDAAQRALAGGFBYPYDDLD
RIWKTVLLHOGHDILGGSSIAWVHREARATYDRVAAFELWGIIDAGAVRALAGEGDTPLV
FNSAPHARAGVPAGAAASPATDGRTGLSPRFGGGHVLDNGLKVEIDEGGLYVSAYDL
AADRETIAPGGAGNILQLHPDFPNMWDAWDVDEFYRNTDLTDADAVRAGRAVR
TUSEFGSSWTOUT IA BGGRBU FUTTEWTUNDEFYRNTDLTDADAVRAGRAVR
TUSEFGSSWTOUT IA BGGRBU FUTTEWTUNDEFYRNTDLTDADAVRAGRAVR
                                                                                                                                                                                                                                                                                                                              Complement(6484. .7731)

/gene-"SCM11.04c"
/gene-"SCM11.04c, hypothetical protein, len: 415 aa;
/note-"SCM11.04c, hypothetical protein Streptomyces
similar to TR:CAB56687 (EMBL:AL121596) Streptomyces
coelicolor hypothetical 71.4 kD protein SCF51A.35, 644 aa;
fasta scores: opt: 205 z-score: 234.7 E(): 1.1e-05; 26.0%
identity in 408 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCM11.03c, possible alpha-mannosidase, len: 1007
aa; similar to TR:AAC00190 (EMBL:AF044414) Homo sapiens
alpha-mannosidase 6A8B, 1062 aa; fasta scores: opt: 1326
z-score: 1446.5 E(): 0; 37.8% identity in 1013 aa overlap
and to SW:MANI_RAT (EMBL:M57547) Rattus norvegicus
alpha-mannosidase (EC 3.2.1.24), 1040 aa; fasta scores:
opt: 1285 z-score: 1401.8 E(): 0; 35.9% identity in 1041
/translation="mpsavrfgvnytpsvgwfhhwldfdldsvradldsiaaldvdhy
RVfflwpyfqpnrtlireravedlvalvdaagergldvnvdglqghlssfdyvpawtr
TWHRRNLfTDPDVVEGQaaylrtlaaalagrpnflgwtlgnevnqfsagphpdpdrat
                                                                                                                 /product="hypothetical
/protein_id="CAB61915.]
/db_xref="GI:6522834"
                                                                                                                                                                                                                                                                                                                     rasta scores: opt:
identity in 408 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6350..6353)
complement(6484..7731)
/gene="SCM11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVAPLVTVDRDAVVVTAVKLADDGSGDVVVRFHEAHGGRTRATLTAGFAVADVQVTDL
LERPLADTEAPRPDGDRIAVSLRPFQLTTLRLKRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVRSFGSSRVTQVLTLAPGERRLEVDTEVDWHETEKFLKLAFPLDVHAERYASETOFG
HFHRPTHTNTSWEAAKFEACNHRFVHLEEPGWGVALVNDSTYGHDVTRTVRTDADAGT
TTTVKLSLLRAPRFPDPETDQGVHRFRHALVPGAGIGDAVREGWRINLPERHLTGGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative alpha-mannosidase"
/protein_id="CAB61914.1"
/db_xref="GI.6522833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           z-score: 149.8 E(): 0.58; 27.7% identity in 166 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aa overlap"
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/gene="SCM11.03c"
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RYEVVIEGTADEVARKDGDWREYEFKGKPGDPRRWPRQFAPYHLRLDWLMWFAALSPS
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WLVPWALYLSIVNVGQTWYSFGWESLLLETGEVAAVELGNEEVAAPVVVLETLEWILLER
VEEGAGLIKWRGDECWRKLTCLDHHEETOPMEGPLSWEFHHLDKPLHKVEVAANHVTO
LVVPFLLEAPHPVSTAAAALMIATQLWLVLSGNESWLNWVTIVLALSVVREPADAPSV
                                                                                                                                                                                                                                                    /transl_table=11
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complemen+/2011
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/protein_id="0AB61913.1"
/db_xref="GI:6522832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
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Best Local Similarity
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 gcccgctccaccatccctacggcaaccgggagctctggaggaaggtggggacggtcgtc 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcaccaaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    carotenoid dehydrogenase; cell division protein; DNA-binding protein; ftsI; ftsQ; ftsW; ftsZ; isoleucyl-tRNA synthetase; lipoprotein signal peptidase; metF; methylenetetrahydrofolate reductase; methyltransferase; murD; murE; murE; muxC; muxX; Na+/H+ antiporter; peptidoglycan biosynthesis; pseudouridine synthase; sporulation protein; thiamin phosphate pyrophosphorylase;
                                                                                                                                                        A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Streptomyces coelicolor cosmid 4A10.
  James, K.D.,
                                                                             Saunders, D.C.
                                                                                                                                    9700035
                                                                                                                                                                                                                                        Kinashi, H. and Hopwood, D.A
                                                                                                                                                                                                                                                                 Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL109663.1 GI:5689939
                                                 Unpublished
                                                                                                                                                                                                                                                                                                                     Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptional regulator.
                                                                                                                                                                                                                                                                                         (bases 1 to 43147)
                        (bases 1 to 43147)
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complement(7763. .8683)
/gene="com"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Binding-protein-dependent transport systems inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Binding-protein-dependent transport systems inner membrane component and to Prosite entry {\tt PS00402}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SCM11.05c, probable transport system permease
protein, len: 306 aa; similar to TR:P73854 (EMBL:D90910)
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/note="SCW11.05c"
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  Parkhill,J.,
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                                                                                and Harris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 174;
  Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 34983;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Blbb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-1999) Streptomyces coelicolor sequencing projestanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 4AIO Lies between and overlaps with cosmids 4G6 and 2C1 the AseI-C genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most-upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strand)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SC4A10.01, hypothetical protein, partial CDS, >67 aa; unknown function, probable CDS suggested by frameplot and positional base preference. Continues cosmid 4G6 as SC4G6.39"
                           /note="SC4A10.02c, hypothetical protein, len: 196 aa; unknown function, probable CDS suggested by GC framepl positional base preference and amino acid composition Annotated in cosmid 466 as SC4G6.38c"
                                                                                                                                                             /gene="SC4A10.02c"
complemen+/100
                                                                                                                                                                   complement(190.
                                                                                                                                                                                                                  complement(190.
                                                                                                                                                                                                                                             SEWTRSYRTRSGTORVERVYSPA"
                                                                                                                                                                                                                                                                                                  /product="hypothetical
/protein_id="CAB51977...
/db_xref="GI:5689940"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Streptomyces
/strain="A3(2)"
                                                                                                         /gene="SC4A10.02c"
/note="SC4A10.02c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SC4A10.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="overlap with Streptomyces coelicolor cosmid 4G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC4A10.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                            /translation="IRAANRHVRWVDTDRHGYGVLDITADRAQMDYYVVSDRTDPRAT
                                                                                                                                                                                                                                                                                                                                                                                  /label=SC4A10.01
                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cosmid 4Al0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "SC4A10.01"
                                                                                                                                                                                                                                                                                                                           7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor A3(2)"
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9

frameplot,

len:

CDS

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/note-*SC4A10.03, possible membrane protein, len: 382 aa; unknown function, shows weak similarity to parts of many hypothetical proteins e.g. Sw:YB83_METJA (EMBL:167556) Methanococcus jannaschii hypothetical protein (361 aa), fasta scores; opt: 222 z-score: 255.3 E(): 6.7e-07, 24.8% identity in 306 aa overlap. Contains hydrophobic, possible membrane-spanning regions. Contains Pfam match to entry pr00924 upp0003, Uncharacterized protein family UPF0003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative Na+/H+ antiporters e.g. SW:YU23_MYCTU (EMBL:.277163) Mycobacterium tuberculosis putative Na(+)/H(+) exchanger (542 aa) (31.4% identity in 528 az overlap). Shows weak similarity to SC66T3.14c (EMBL:AL079348) S.coelicolor probable Na(+)/H(+) antiporter (514 aa) (27.5% identity in 545 aa overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2056. 3642)

/gene="SC4A10.04c"
/gene="SC4A10.04c"
/note="SC4A10.04c, possible Na+/H+ antiporter, len: 528
/note="SC4A10.04c, possible Na+/H+ antiporter, len: 528
aa; shows weak similarity to the N-terminal portion of
eukaryotic Na+/H+ antiporters e.g. SW:NAH3_RAT
(EMBL:M85300) Rattus norvegicus sodium/hydrogen exchanger
3 (831 aa), fasta scores; opt: 271 z-score: 293.1 E():
5.3e-09, 25.8% identity in 481 aa overlap. Similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="METILRPLIVVGGSVLLTVVIGWATDLLLRKADGRHPETPLWGL
LRRARVPYQIVLCSGLLRGSVYEAGVFFEHRTGYGRTLTLLLGSWALLVTFAMRAAGAS
ETSYSRYAHAHAERDPARVRFVRTQVSLLMRVVTAVVGVVAVSSMLLTFBAMRAAGAS
LLASAGIIGIVAGVAAQSTLGNLFAGFQIAFGDMVRMGDTVVVDGEWGTVEEITLTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SC4A10.03"
886. .2034
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LHGTSDLAPNASVDELPVQLHVAEPDPFETDDWLSAWYLQMGRIGADVEVHRYPGAGH
                                                                                                                                                  /translation="MDQLALLFMLLLGALLSVPIGARLGLPAPVLMTLLGIVLALLDF VPNVD)IPPELTLPGLLPPLLYAAVRRTSWRQFAANKRFLFLEXVALVEYWWCYASVA HAIVFGLPIAAAFALGALLVAPPDPVAATAVAGQLGLPRRLYSILEGEGLFNDVTAIVLY YHVAIAAAVGGSFSPWRAGFDLVLSAVVAVAIGLIVLGWGSNKLMSVLGDPTLQIGITL YLVAIAAAVGGSFSVPRAGFDLVLSAVVAVAIGLVLGWGSNKLMSVLGDPTLQIGITL YUPFVSYVAADELHGSGVLAVLTTAMFLAEYASDADDVMTRLGGHTVMDVVDTILVTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains hydrophobic, possible membrane-spanning regions. Contains Pfam match to entry PF00999 Na_H_Exchanger, Sodium/hydrogen exchanger family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SC4A10.04c"
complement/2077
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/note="Pfam match to entry pF00924 UPF0003,
/note="Pfam match to entry UPF0003, score 15.70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVRTWDERRITMPVSYFTSKPFENWSRGTPQMTGTVFWHLDHSAPMDLMRERLRDILR
ECPAWDGRNYNLTVTDTTPTTMEVRALVTAKDADDIWTVRVTVREGMLRWLADEHPYA
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/product="putative membrane
/protein_id="CAB51979.1"
/db_xref="GI:5689942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical
/protein_id="CAB51978...
/db_xref="GI:5689941"
                                                                                                                                                                                                                                                                                                                                                 /product="putative Na+/H+ antiporter"
/protein_id="CAB51980.1"
/db_xref="GI:5689943"
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                                                                                 DEDIPTSWRETVVMWWAGMRGVASVALALAIPLETDDGAAFPHREEIVFIAFGVIMGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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QMLRRAFDIGIRISPDLGDEERREAQEQRARRIKRVRRIQGEMLSAARHEVLAARSEP
                                                                                                                      AFGLIGLELHNAVRTASGRWTELLGWAAAILVVVVLVRLLWLLPATWLTQRLHARRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/label=SC4A10.04c
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AF357202
KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtccacgcctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttca 506
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                                                                                                                                                                                        CCGCCCCTGGTTCGCGATCGGCGCATCGACCTCGGCAACCTGGACGAGG 42179
                                                                                                                                                                                                                         cccggcccttatcaccctcattgctacgtacattgccgatctcctagatg 856
                                                                                                                                                                                                                                                                 gaccgtggccgttgacctgggcctcatcctggtcctccccgaggtggagcgttccaaact 806
                                                                                                                                                                                                                                                                                                                                          CGCGGCCCAGGAGGGTGTGGACTACTTCTGCACCGGCCCGTGCTGGCCGACCCCACCAA 42289
                                                                                                                                                                                                                                                                                                                                                                ccccaccctggacgtgctggtcctctgggctcaggggaaaagggtgatgcccaacaccaa 746
                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCGGCGACGACGTGCTGATCGGCCGCTCCACGCACGCCGAGTCCGAGGCCGCCGCCGCGC 42349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agggaaagccaggctcaccctggacgactacatctacccctggaggaacctcgccctaga 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGGACAAGGGAATGGAGGCGGCGGAGGAACTGGAGCACCTGGCGGTCTTCGCCGACGC 42529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209;
                                     Streptomyces nodosus amphotericin complete sequence. AF357202
                   AF357202.1
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/note="SC4Al0.05c, hypothetical protein, shows weak similarity to hypothetical
proteins from other eubacteria e.g. SN:YYBD_BACSU
(EMBL.D26185) Bacillus subtilis hypothetical protein (147
aa), fasta scores; opt: 199 z-score: 236.4 E(): 7.6e-06,
36.8% identity in 144 aa overlap. Shows weak similarity to
SC5F7.12c (EMBL:AL096872) S.coelicolor possible
acetyltransferase (169 aa) (37.7% identity in 114 aa
overlap). Contains Pfam match to entry PF00583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3731. .4213)
/gene="SC4A10.05c"
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complement/???
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry PF00999 Na_H_Exchanger, Sodium/hydrogen exchanger family, score 258.90, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="CAB51981.1"
/db_xref="GI:5689944"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SC4A10.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MPSRAPAAYEVRVAEDPVDREACFAVRKDVFVAEQKVPEDIEYD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=SC4A10.05c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52.4;
                                                                                             113193
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                                                                           biosynthetic gene cluster,
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                                                                                                 BCT 17-JUL-2001
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JOURNAL REFERENCE
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TITLE
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Caffrey, P., Lynch, S.V., Flood, E.M., Finnan, S.M. and Oliynyk, M. The amphotericin biosynthetic gene cluster from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces nodosus.
Streptomyces nodosus
Bacteria; Firmicutes;
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Caffrey, P., Lynch, S.V.,
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                                                                                                                                                                                                                      164;
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                     5.1%;
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                                                                                                                                                                                                                                                         186;
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REFERENCE
AUTHORS
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KEYWORDS
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AL646072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15813 CCCCCAACGGCCCCTCCCAGCAGCGCGTCATCCGCCAGGCCCTGGCCCAAC 15862
                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Arlat,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Chandler,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Sjuuier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INRA, BP27, F31326 Castanet-Tolosan Cedex
Christian.Boucher@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, Fran Laboratoire de Biometrie et Intelligence Artificielle INRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siguier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M., Weissenbach, J. and Boucher, C.A.
Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum
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AL646072 AL646052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://sequence.toulouse.inra.fr/R.solanacearum.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boucher, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalstonia.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 188050)
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                                                                                                                          /translation="MLALLGSMASVCVGNSFAKTLFPALGAAGTVYRITIGAAILLA
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73. .909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:17429824
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(SMALL CHAIN) OXIDOREDUCTASE PROTEIN"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /EC_number="1.17.4.1"
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metabolism; 2-prime-deoxyribonucleotide metabolism"
/note="Product confidence : putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (3477. .6440)
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/gene="nrdA"
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/note="Product confidence : putative
Gene_name_confidence : putative
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predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="RSC2803"
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Gene name confidence: hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAGALFPAVEKTVITLEFGTLEPMAVMQALRADHWLHRHPGTSPDQAAAIRKGLRDAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGALSWD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="RSc2804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene≖"nrdB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl/
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                                                                                                                                                                                                                                                                                                                                                                                transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  name confidence :
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d by Homology
d by FrameD"
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Matches Query Matc Best Local

187;

Conservative

0;

198;

6

Gaps

Similarity

5.1%; 47.8%;

Score 52.2; Pred. No. 4; Mismatches

DB 1;

Length 188050; Indels

Db 140037

447

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SDIAPGRKTDGGFTDWAHLRLAKLEAALFPYQAGAAPA"
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CNIRSPQQHVGVVHSSNLCTEITLNTNDSEIAVCNLGSVNLVAHVVKQADGSYALDHD
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SNLSGEFTVWNDYLVRDLKARGLWDSVUNVADLKYFDGGSLARIDRIPQDLBLYATHGE
VEPQWLVEAASRRQKWIDQAQSLNIYMAGASGKMLDDTYKLAWLRGLKTTYYLRTIGA
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GVPQPVGGWPDAAYIPVPVPMGLMPHPVVVPVPVEPAPVIEPAAPAMPAVSLPVDLPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="small molecule global regulatory function
                                                                                                      VRKIGESREDPVDVRVVCASHQNLARLVAAGRFREDLFYRLNVLELRMPTLRERAEDV
PVLAGVLLEQLAARYGDLRPKRLTRQALQQLCAYPFPGNVRELDNLLERAYAFAEGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7472. .9184)
/gene="pehR"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /product="probable response regulator transcription
regulator protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /_uuction="smail molecule metabolism; global functions; global regulatory functions"
/note="Product confidence: probable
prodicts & confidence: probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7472. .9184)
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detoxification"
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LSKFAGGLGNDWTNVRALGSHIKGTNGKSQGVVPFLKVVNDTAVAVNQGGKRKGAVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="RSc2807;
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Search completed: May 29, 2002, 10:21:27 Job time: 7259 sec

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Thermus plasmid pT
SOD-T gene. Therm
Zea mays neoxanthi
HSV-2 strain SB5 C
HSV-2 strain SB5 C
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207377-в1	67	Thermus sp.	Replication kanamycin-r replication	rmus repl	Thermus rep	04-JUL-2001	AAD04666;	1		⊢ ⊢	41.8	<u></u>		٠,	۷.	2		2 2 5	2 .		42.8 42.8	4-4	43.4	ω.	43.6	44	٠. ۵	4	44.8	ÿ	5	<u>ب</u>	45.6
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	s tion aa:Me		partition protein; ParA; thermophilic transformat	RepT encoding DNA			BP.	ALIGNMENTS	ABA26979	AAT80414	AAV26609	AAH26469	AAV84455	AAA584/1 AAO94255	AAS92733	AAZ40194 AAT51330	AAH01758	AAA14651 AAV37167	AAV25925	AAQU6631 AAT93095	AAD17186	AAA64890	AAQ63293	AAA47070 AAA64885	AAV23288	ABL22159	AAS54251	AAA/15/1 AAA93444	AAC43669	AAV62134	AAS54366	S	
	RepT		ParA; pTsp45S plasmid; ormation; Ori;	from pTsp45S plasmid.					Probe #5445 for ge	_	Actinomadura hibis Platenolide syntha	Ancestral HIV-1 gr	Human secreted pro	Nucleotide sequenc	DNA encoding nove	Human Na+/H+ excha	Thiomonas cuprina	DNA sequence used	S	Gene conferring te Streptomyces freno		·	Sequence encoding	cDNA sequence of a Bordetella pertuss	Synthetic human Fa	Drosophila melano	Pseudomonas aerug	s. aggregatum rns GFP-HSF1 fusion ge	ea mays DN	HSV-2 strain SB5 C	Pseudomonas aeruc	groEL-1 gene codin	

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Thermus sp.

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Key

FT

CDS

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CDS

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/*tag= a

FT

/product= "Replication protein, RepT"

/prodon= (Seq:GTG, aa:Met)

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US6207377-B1.

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US6207377-B1.

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PD

27-MAR-2001.

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PR

14-AUG-1998; 98US-0134246.

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CC needed for thermophilic plasmid protein relates to the invention relates to Thermus sp. replication protein RepT, partition protein ParA and their corresponding DNA molecules which relates to recombinant DNA molecules encoding plasmid DNA replication origins in Thermus, as well as to shuttle vectors which contain the same. The green which comprises inserting plasmid DNA comprising a Thermus sp. plasmid genes which comprises inserting plasmid DNA comprising a Thermus sp. plasmid origin of replication (Ori) into a recombinant plasmid comprising a thermostable kanamycin-resistance gene and an Escherichia coli Ori, to produce a cloned recombinant plasmid. This cloned recombinant plasmid is transformed with an E. coli host cell, and E. coli host cell cultured for the expression of cloned recombinant plasmid. The cloned recombinant plasmid isolated from E. coli host cell, so the transformed with Thermus sp. plasmid genes are cloned. These plasmid DNAs are used for thermostable transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1026; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning Thermus species (Ts) plasmid genes comprises transforming Escherichia coli with cloned recombinant plasmid containing Ts and E.coli origins of replication, isolating cloned recombinant plasmifrom E.coli and transforming Ts cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1026 BP; 221 A; 323 C;
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Cloning Thermus species (Ts) plasmid genes comprises transforming Escherichia coli with cloned recombinant plasmid containing Ts and E.coli origins of replication, isolating cloned recombinant plasm from E.coli and transforming Ts cell

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Matches 1026; Conserv
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The invention relates to Thermus sp. replication protein RepT, partition protein ParA and their corresponding DNA molecules which relates to recombinant DNA molecules encoding plasmid DNA replication origins in Thermus, as well as to shuttle vectors which contain the same. The invention also relates to method useful for cloning Thermus sp. plasmid genes which comprises inserting plasmid DNA comprising a Thermus sp. origin of replication (Ori) into a recombinant plasmid comprising a thermostable kanamycin-resistance gene and an Escherichia coli Ori, to produce a cloned recombinant plasmid the produce a cloned recombinant plasmid to the plasmid to the produce a cloned recombinant plasmid to the produce a cloned recombinant plasmid to the plasmid to th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produce a cloned recombinant plasmid. This cloned recombinant plasmid is transformed with an E. coli. host cell, and E. coli. host cell cultured for the expression of cloned recombinant plasmid. The cloned recombinant plasmid isolated from E. coli host cell is then transformed with Thermus sp. host cell and Thermus sp. host cell and Thermus sp. plasmid genes are cloned. These plasmid DNAs are used for thermophilic transformation.
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aaggcctaccaggaccacggaatccgccccaccctggacgtgctggtcctctgggctcag
                                                                        tacccctggaggaacctcgccctagacatggccaacggcgtgctctccttcaactgggtc
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                                                                The sequence shown is that isolated from Thermus aquaticus genomic DNA and encodes a heat resistant super oxide dismutase enzyme. The gene is useful for medicines for inflammation and as a protection against X-rays, as a reagent for research in enzyme electrodes or a
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                                                                                                                                                                                                                                          Gene, of and plasmid contg. heat resistant super:oxide dismutase - for treating inflammation, X=ray protection, enzyme electrodes
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    Sequence
                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                               P-PSDB;
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DB; AAR32376.
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    A; 223
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Query Match Best Local Similarity

47.5%;

Score Pred.

54.4; DB 14; No. 0.0023;

Length 615;

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ARESULT
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  Claim
                                 A DNA encoding a protein with a neoxanthin cleavage activity producing transgenic plants with improved or decreased stress
                                                                                                                                                       13-JAN-2000; 2000JP-0010056
11-JAN-2001; 2001JP-0003476
                                                                                  WPI; 2001-400081/43
                                                                                                        Iuchi S,
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                                                                                                                                                                                                               18-JUL-2001.
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                                                                                                                                                                                                                                                                                                                       Zea mays
                                                                                                                                                                                                                                                                                                                                            plant growth protectant;
                                                                                                                                                                                                                                                                                                                                                     Malze; neoxanthin cleavage enzyme; VP14; abscisic acid; ABA; herbicide; stress tolerance; transgenic plant; plant breeding; antisense-therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2001
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                                                                                                                               (RIKE )
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                                                                                                                                RIKEN
                                                                       AAE04788
                                                                                                        Kobayashi
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60-64; 101pp; English.
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Best Local Similarity 45.9
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to neoxanthin cleavage enzymes and their corresponding cDNA molecules. Neoxanthin cleavage enzyme plays a key role in endogenous abscisic acid (ABA) biosynthesis under drought stress. Neoxanthin cleavage enzyme is used for improving stress tolerance in a plant when expressed in a plant cell. The invention also relates to methods for increasing or decreasing stress tolerance in a plant by introducing the DNA into the plant, and a transgenic plant into which a neoxanthin cleavage enzyme is introduced. The improvement of stress tolerance in plants is useful, for example in plant breeding. Neoxanthin cleavage enzyme genes are useful for producing transgenic plants. An arid then removing the weed by growing transformant weed for several years and then removing the weed by specifically lowering stress tolerance in the weed by inducing an inducible promoter. The present cDNA sequence encodes recent and the control of the control of the sequence encodes are useful for several plants.
                                                                                                                                     HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                    HSV-2 strain SB5 Contig ID 10 DNA sequence
                                                                                                                                                                                                                         18-DEC-1998
                                                                                                                                                                                                                                                          AAV62154;
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                                                                                                                                                                                                                         (first entry)
                                                                                                     virus
                                   complement (1..5672)
/*tag= a
                   /transl_except=
                                                                    Location/Qualifiers
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45.9%;
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xcept= (pos: 1..2,
"ORF#1 protein"
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Pred. No. 0.013;
""matches 209;
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                   aa: Thr-Xaa-Xaa-Xaa-Xaa-Xaa)
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Best Local Similarity 43.
Matches 207; Conservative
                                                                           This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 10, and encodes 8 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
                                                                                                                                                                                                                         Herpes simplex virus type-2 sequences - and treatment of infection or inducing
                                                                                                                                                                                                                                                             WPI; 1998-286847/25.
P-PSDB; AAW72095, AA
AAW72101, AAW72102.
                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                    Chan JY,
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04-NOV-1996;
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                                                        21034 BP; 3154 A; 7419 C;
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Leary JJ;
                                                                                                                                                                                          350-359; 748pp; English.
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96US-0030279.
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/product= "ORT#8 protein"
/note= "encoded protein _____
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/product= "ORF#7 protein"
/note= "encoded protein s
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/note= "encoded protein s
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/note= "encoded protein s
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                                                                                                                                                                                                                                                                       AAW72096,
            4.7%;
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unspecified amino acid"
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 Score 48.6; D
Pred. No. 0.12
0; Mismatches
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                                                       7234 G;
           6; DB 19;
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                                               /product= "ORF#5 protein"
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6017..8482
/*tag= f
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/note= "encoded protein s
complement (3130..3735)
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complement (3802..6447)
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/note= "encoded protein shown
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ication; viral protein inhibitor;
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                                             Human herpesvirus 2; cytostatic; cancer; immunosuppressive; virucide; antihacterial; fungicide; protozoacide; antirheumatic; antiinflammatory; antiarthritic; rheumatoid arthritis; neuroprotective; multiple sclerosis; immune response; vasotropic; vaccine; gene therapy; autoimmune disease;
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                     Human herpesvirus
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                                                                                                                                                                                                                                        CAGGCGCTGGCGGGACGCACGCGCTACAACCCCCGGGACTTCCGCAAGCGC
                                                                                                                                                                                                                                                              ctggtcctccccgaggtggagcgttccaaactcccggcccttatcaccctc
                                                                                                                                                                                                                                                                                    GCGGCGCTGGACCGCGTCGAGAACCGCGCGAGTTCGACGTGGTCGAGCTGCGCCGCCTG
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                                                                                                                                    (first entry)
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/note= "encoded protein shown
complement (58060..58977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60759..61151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (58970..60760)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
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The invention relates to a composition comprising an expression vector CC bound to an aggregated protein-polycationic polymer conjugate or CC suspension. The expression vector contains a promoter polynucleotide sequence operatively linked to a polynucleotide sequence encoding an CC infectious disease, cancer and autoimmune disease such as rheumatoid CC arthritis, vasculitis, and multiple sclerosis, pathogenic genomes CC immunodeficiency virus (HTV), herpes simplex virus (HSV), hepatitis C virus (HCV), influenza and respiratory syncytial virus (RSV), and CC optionally comprising a nucleotide sequence encoding a tropic contains a sequence for granulocyte macrophage-colony stimulating factor CC (systemic and/or mucosal) in an organism. The cytokine expression vector contains a sequence for granulocyte macrophage-colony stimulating factor the antigen and the cytokine are under transcriptional control of same or CC different promoter polynucleotide sequences. The expression vector, as a DNA vaccine is useful for treating a condition in an organism. The CC present sequence is human herpesvirus 2 complete DNA genome related
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 90-132; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing antigenic protein-polycationic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FM, Kinsey BM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for oral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       delivery of vaccines, comprises expression vector genomic sequence, bound to aggregated polymer conjugate or suspension -
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Sequence 154746 BP; 23003 A; 54218 c; 54701 G; 22824 T; 0 other;

4.78;

Score 48.6; Pred. No. 0.

DВ

24;

Length 154746

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nes 207; Conserv
                                               GCGAAGATGGCGCCCAGCGCCCCGGGGCAGCAGCGAGCGCTGGGCCGCCGGCGTCGAG
                                                                                                              GTCATCGGCGCCACGCGACGCCGCCGACGAACTTGAGGCCGCCGTCGCCGACCTGACG
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                                                                                                                                                                                                       atcygcaccctttgggccgtccggctgaggccagggaaagccaggctcaccctggacgac 594
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                                                                       tgggtcaaggcctaccaggaccacggaatccgcccaccctggacgtgctggtcctctgg
                                                                                                                                         tacatctacccctggaggaacctcgccctagacatggccaacggcgtgctctccttcaac
                                                                                                                                                                                                                                         ACGACCGCTGCTCGGGAAAGCCTCGCGGGGGCACGAGGCTGGGTTCGGGGGCCCTGCTGCAC
                                                                                                                                                                                                                                                                      aaaaaagggcctggtggccaccgacgtccttcaccaaaccgtcaacggggagcgccgggcc
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76872 CAGGCGCTGGCGGCACGCACGCCTACAACCCCCGGGACTTCCGCAAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Selecting monoclonal antibodies, by expressing them on the surface of hybridomas attached to antibody-binding protein, then reaction with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAB10432, AAB10437, AAB10438
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                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 1; 22pp; German
              vector pSEX11L4 encoding protein G, used in the method of the invention
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oma cell; hybridoma; protein G; bla protein; ds.
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19-DEC-1997;
14-MAR-1997;
14-MAR-1997;
30-MAY-1997;
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                                                                                                                                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                  endocrine; metabolism;
                                                                                                                                                                                                                                                                                         Human secreted protein gene 13 clone HNFCV70.
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 97US-0040710.
97US-0040762.
97US-0048100.
97US-0048189.
97US-0048357.
                                                                                      98WO-US04858
                                                              97US-0068368
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44.18;
                                                                                                                                                                                     regulation; malabsorption; gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to CC generate fusion proteins by linking to the gene to a human immunoglobulin CC Fc portion (e.g. AAV34277) for increasing the stability of the fused CC protein as compared to the human protein only.

CC rate invention relates to 28 novel genes and their fragments (nucleic CC acid sequences: AAV34286-V34325; amino acid sequences AAW75196-W75235) CC which are useful for preventing, treating or ameliorating medical CC conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 28 CC polypeptides in a sample or by determining the presence of mutations in CC conditions, based on which tissues they are most highly expressed in CC (see AAV34286 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
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06-JUN-1997;
05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated human poly:nucleotide(s) encoding secretory peptide(s) used to develop products for the diagnosis and treatment of e.g. inflammation, cancers, CNS disorders or immune system disorders
        403
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Li H, Li Y,
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GCGGCTGAGTCCGGTACCCTCTAAGTGGCCCCTGGTAGAAGCAGTGGTCCTGCCCGCGAGG
                         atycccaacaccaagaccgtggccgttgacctgggcctcatcctggtcctccccgaggtg
                                                                                     gaccacggaatccgccccaccctggacgtgctggtcctctgggctcaggggaaaagggtg
                                                                                                                      TGCTCAGCCTGGTACACGGCGTGCCGTCCGCCCTCGCCACCTTCATCCAGGGGGCTCGATC
                                                                                                                                           aacctcgccctagacatggccaacggcgtgctctccttcaactgggtcaaggcctaccag
                                                                                                                                                                                CCCAGGAGGCTGCCCAGGCTGTCGCTGACCCCGCAGGTCCCGGCCGTCTGCAGCAGG
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DB; AAW75227.
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97US-0048970.
97US-0057765.
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Pred. No. 0.23
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SM,
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289 gtccaggacgggcctcagaagcttctggaactcctccaggagattgcccgctccaccatc

Query Match 4.4
Best Local Similarity 43.1
Matches 219; Conservative

4.48; 43.18;

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Score 45.6; DB Pred. No. 0.33; 0; Mismatches

289;

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RESULT 10
AAQ224482
ID AAQ224
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                                              The sequence is that of the coding region of the groEL-1 gene which codes for the 18 kDa heat shock protein HSP18. The gene actually codes for a 56 kDa protein but this is subjected to post translation modifification to give the 18 kDa HSP18 protein.

See also AAQ22477-Q22486.
  Sequence 1620 BP;
                                                                                                                                                                                                                   Claim 18; Fig 8; 50pp; French.
                                                                                                                                                                                                                                                                  Recombinant DNA contg. heat inducible promoter gene - also vectors, transformed cells and new proteins of Streptococcus albus
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-114358/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1992
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Best Local Similarity 43.1%;
Matches 219; Conservative
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                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
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21-MAR-2000; 2000US-191078P
                                                        21-MAR-2001; 2001WO-US09180
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                                                                                                                                                                                                                             Pseudomonas aeruginosa
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ARESULT 13
AAV62134/C
ID AAV62134 standard; I
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AC AAV62134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonelia typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in CC avide variety of organisms. The present sequence encodes an CC usesential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
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Best Local S
Matches 134
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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DB; AAU36507.
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; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
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Xu HH;
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identification; viral
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/note= "encoded protein shown
complement (17295..19110)
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/note= "encoded protein s
complement (6263..6745)
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/note= "encoded protein s
complement (9721..13911)
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/note= "encoded protein s
complement (8386..9477)
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/note= "encoded protein s
complement (3637..6093)
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/note= "encoded protein sh
complement (19111..20064)
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              /product= "ORF#15 protein"
/note= "encoded protein shown
24286..25632
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/note= "encoded |
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/note= "encoded protein sh
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/note= "encoded protein sh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 104, and encodes 17 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological response in a mammal.
                                                                                                                                                                                                                                                                    2382
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04-NOV-1996;
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                tacatctacccctggaggaacctcgccctagacatggccaacggcgtgctctccttcaac
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96US-0030279
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/product= "ORF#17 protein"
/note= "encoded protein shown
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01-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein identification; signal transduction pathway;
pathway; promoter; termination sequence; corn; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays DNA fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC43669
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9905-0134256

9905-0134218

9905-0134211

9905-013470

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990S-0130077
990S-0130449.
990S-0130510.
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990S-0131449.
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99US-0127462.
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                                 Query Match
Best Local Similarity 47.
Matches 137; Conservative
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                                          4.48;
                                ; Score 45.2; D; Pred. No. 0.38
                                           .38;
                                                    Length
                                  0;
                                  Gaps
 135
                  538
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16-JUN-1999
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99US-0139119.
99US-0139452.
99US-0139454.
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99US-0139456.
99US-0139460.
99US-0139460.
99US-0139461.
99US-0139463.
99US-0139763.
99US-0140354.
99US-0140354.
99US-0140823.
99US-0141284.
99US-014286.
99US-0144286.
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99US-0145918.
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99US-0146388.
99US-0147303.

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This invention describes novel DNA sequences encoding for polyketide C(PK)-like synthesis (PKS-like) pathway genes from Shewanella, Vibrio and Schizochtrium. The nucleic acids are useful for isolating related molecules or in methods to detect organisms expressing the PKS-like poly-unsaturated long chain fatty acids. The poly-unsaturated long chain fatty acids. The poly-unsaturated long chain fatty acids are useful as dietary supplements for fatty acids produced recombinantly are useful as dietary supplements for malnutrition. The poly-unsaturated long chain fatty acids can also be incorporated into cooking oils, fats or margarine formulated so that in commal use the recipient receives a desired amount of poly-unsaturated conscious chain fatty acids. The nucleic acids are also useful in large scale production of the fatty acid and elcosapentencic acid, and for the cooking chain fatty acids conscious acid profile of host cells and edible plant cut issues and/or plant parts. Transgenic production of polyunsaturated conscious acids in particular host cells allows quicker purification from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKS pathway; polyunsaturated long chain fatty acid; plant; transgenic; polyketide-like synthesis; PUFA; dietary supplement; intravenous feedi malnutrition; cooking oil; cooking fat; margarine; docosahexenoic acid production; elcosapentenoic acid production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA sequences encoding for polyketide (PK)-like synthesis pathway genes from Shewanella, Vibrio and Schizochtrium, useful for creating transgenic plants that express poly-unsaturated long chain fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Fig 27C1-2; 302pp; English.
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Best Local
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                                                                                                                                                                                                                                                                                                                             3263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  natural sources such as fish or plants. This sequence encodes the Schizochytrium aggregatum PKS protein cluster ORF8/ORF9 homolog of clones LIB 84-015-D5, LIB 81-042-B9 and a bridging PCR product
                                                                  3503
                                                                                                                                                                                                                                                                                                                                                                                            3203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395
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hes 222;
                                                                                 ccgttgacctgggcctcatcctggtcctccccgaggtggagcgttccaaactcccggccc
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tcaccccgcaggtcgtgcgctaccgcgccgccggcct
                              ttatcaccctcattgctacgtacattgccgatctcct
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ALIGNMENTS

REFERENCE AUTHORS TITLE KEYWORDS SOURCE RESULT 1 CNS0091P/c LOCUS FEATURES COMMENT DEFINITION VERSION ACCESSION ORGANISM JOURNAL source AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Direct Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BBGP). The BBGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BBGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BBGP from the isogenic strain y2; cn bw sp, the same strain used for the BBCP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 925) מע כבל DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ALOS3013 GSS Genoscope AL053013.1 fruit fly. /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98" Location/Qualifiers GI:4934461

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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                                                                                                                                                                                                                       J., Oates,R. and Main,D. Development of a genetically and physically anchored for barley genomics: Morex rachis cDNA library Unpublished (2001)
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rar
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                      Clemson University
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 249 c 158 g 105 t
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/db_xref="taxon:4513"
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/lab_host="TJC121"
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/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genome.clemson.edu/projects/barley. To order
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM335757 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 515-294-2299
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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515-294-0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        State University
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pT7T3PAC; Site_1: ECORI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patrick S. Schnable
                                                                                                                                                                                                                                                                                   (1-aminocyclopropane-1-carboxylix acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscisc acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, GA (Jasmonic acid)-treated seedlings, GS-cDNA molecules were generated as follows. First-strand cDNA was
                                                 resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the
                                                                                                                                                                                                         prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MEST160-F05"
/clone_lib="ISUM5-RN"
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/cultivar="B73"
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NotI sites of the pT7T3PAC vector. through one round of normalization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccctggacgactacatctaccc 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccctggagatgttggccctcaacctgggggtcacccggcagaccgtccacgcctggaaga 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGCCGGGACTGGGACATCGACTACGAGCTCCAGGTCGGGCTCACCGTCGACCTCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF259495 759 bp mRNA linear EST 22-OCT-2001 HVSMEf0019H19f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0019H19f, mRNA sequence.
                                                                                                                                                                                                                                                                                          100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                          YI., Henry D., Palmer,M., Rambo,T., Simmons,J., VIIII., CALLER, R. and Main,D.
R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource Development of a genetically and physically anchored EST resource.
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                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
Total hq bases = 388
                                                                                                                                                                                                                                                                                                                                                  Clemson University
                                                                                                                                                                                                                                                                                                                                                                       Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                  On Nov 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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/db_xref="taxon:4513"
/clone="HYSMEf(0019H19f"
/clone_lib="Hordeum vulgare seedling root
/robNA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
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122 c 162 g 110 t 13 others
                                                                                                                       /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                   ocation/Qualifiers
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49.2%;
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Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                 29634, USA
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DEFINITION
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Best Local Sim
Matches 162;
                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 gaccgtggccgttgacctgggcctcatcctggtcctccccgaggtggagcg 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 CTACCGCGACTTCGTNCTCGACCTCAACAAGGCCCTCGCCGCCGACCAGCG
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                                                                                                                                                                                                                                                               AV436476 Porphyra yezoensis TU-1 PS002f12_r 5', mRNA sequence.
Nikaido, I.,
                                                                                       Eukaryota; Rhodophyta;
                                                                                                                         Porphyra
                                                                                                                                                                                        EST
                                                              Porphyra.
                                                                                                                                                  Porphyra yezoensis.
                                                                                                                                                                                                                 AV436476.1 GI:8591701
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                               (bases 1 to 524)
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                                                                                                                         yezoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
282 c 184 g 133 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this clone see http://www.genome.clemson.edu,
   Asamizu, E.,
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Pred. No. 1.4;
                                                                                       Bangiophyceae;
   Nakajima, M.,
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   Nakamura,Y.,
                                                                                       Bangiales; Bangiaceae;
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Best Local Similarity
Matches 208; Conserv
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949012C11.x1 949 - Ju
Zea mays cDNA, mRNA s
BG946638
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Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000) 20363100 Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yana 1532-3, Kisarazu, Chiba 292-0812,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 463)
                                                                    Zea mays
                                                                                                     BG946638.1
EST.
                                                                                       Zea mays.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1:
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/clone="PS002f12_r"
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Pred. No. 2.3;
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                                                                                                                                                                         TCGTCGGCAACTTCACCATCCC
                                                                                                                                                                                                                                          TCGGCCGGGACTGGGACATCGACTACGAGCTCCAGGTCGGGCTCACCGTCGACCTCCCCA
                                                                                                                                                                                                                                                                                                        CCGCGCTGGAGATCCCCGCCAAGGTGCCCTACGACTTCCTCGTCTCCCTCGTCAGGGACG
                                                                                                                                                                                                                                                                                                                                      aggtccttgagaaaaagggcctggtggccaccgacgtccttcaccaaaccgtcaacgggg
                                                                                                                                                                                                                                                                                                                                                                         GCAAGGAGGTGGCGTCCGGCACCATGCCGGACCCCGGCTGGATCGCCGCCCAGCGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128;
     sequence.
BM332294
BM332294.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanford University
855 California Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biological
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                                                                    BM332294
MEST154-H06.T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       //dev Stage="4 stages from 3-13 days after imbibing"
//lab_host="E. coli XLOLR"
//note="Organ: juvenile vegetative shoots; Vector:
pAD-GAL4-2.1; Site_1: EcoR1; Site_2: XhoI; Equal amounts
of total RNA by weight from 4 tissue sources (see below)
were pooled, polyA+ RNA isolated, and cDNA synthesized for
EcoRI (5') and XhoI (3') directional cloning into lambda
Hybrizap vector from Stratagene. Tissue Sources: 1. Whole
shoots 3 days after sowing/imbibing in wet soil. 2. Basal
1.5 cm shoots 6 days after sowing includes yellow
portions of developing leaves 1-5, primordia from 6-8, and
the vegetative apex. 3. Non-green portions of developing
leaves 4-5 and the vegetative apex, including adult leaf
primordia, 9 days after sowing. 4. Partially expanded and
greening leaves 4-5 at 13 days after sowing."

79 a 132 c 175 g 77 t
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/cultivar="W64A"
/db_xref="taxon:4577"
/clone_lib="949 - Juver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="immature leaf primordium and vegetative
meristem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                      GI:18162455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%;
                                                                       ISUM5-RN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47.6; DE Pred. No. 2.8; 0; Mismatches
                                                                                                                                                                                                        605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                         97
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                                                                       Zea mays
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                                                                                       539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Juvenile leaf and shoot cDNA from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
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                                                                     mRNA linear EST cDNA clone MEST154-H06
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Indels Length

0;

Gaps

0;

16-JAN-2002 3', mRNA

583

523 239

0;

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BASE COUNT
ORIGIN
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Query Match
Best Local Similarity
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PCR PRIMERS

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (<a href="http://deptts.washington.edu/ventures/collabtr/direct/index.htm>#brt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-Tand the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: schnable@iastate.edu
Individual basecall and confidence value were assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G405 Agronomy, Tov
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wen,T.J., Qlu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Agronomy, Iowa State University, Ames,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //note-"vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
//note-"vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
//note-"vector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
//note-"vector: pT773PAC; Site_1: Site_2: NotI;
//note-"vector: pT773PAC; Site_1: Site_2: NAG), Kernels
//note-"vector: (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG),
//note-rector: Site_2: NAG, Color: Site_2: NotI;
//note-rector: Site_2: Nature ear (0.2-3.0)
//note-rector: Nature ear (0.2-3.0)
//note-rectore
                                                                                                                                             resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT773PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="mixed"
/lab_host="DH10B"
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/clone_lib="ISUM5-RN"
48.98;
   Score
Pred.
47.6;
No. 2
   . 8;
                              10;
                              Length 539;
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Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (<a href="http://depts.washington.edu/ventures/collabtr/direct/index.htm>#brt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                               BACKWARD: Backward PCR primer sequence, primer T3
                                                                                                                                                                                                                                                                                                                                                   CTA TAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Patrick S. Schnable Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                         PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BM075274
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515-294-0975
                                                                                                                                                                                                                                                                                                                                                                        Forward PCR primer sequence,
/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"
                                                                                /db_xref="taxon:4577"
/clone="MEST352-G03"
                                                                                                                                                                      /organism="Zea
                                                                                                                                         /cultivar="B73"
                                                                                                                                                                                                                         Location/Qualifiers
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Matches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agcgccgggccatcggcaccctttgggccgtccggctgaggccagggaaagccaggctca
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                                                                                                                                                                                                             fly), genomic survey sequence. AL108460
                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence SP6 end of BACN37L08 of DrosBAC library from Drosophila melanogaster
                                                                                           Drosophila 
Eukaryota;
                                                                                                                                                                     GSS
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                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                         AL108460.1
Genoscope
                                                                                                                                          fruit fly.
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                        (bases 1 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Sitk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings
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Pred. No. 2.9;
0; Mismatches 134;
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TITLE AUTHORS SOURCE KEYWORDS VERSION В Qy

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASCSSASMCGVSSGSSCSASCGSCCGVSSCSAVSASSASSVMSKVASAVASCSAVASGM 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
             Unpublished (1996)
Contact: Warra W/Mouse EST Project
Washington University School of MedicineP
                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                           AA388278

497 bp mRNA linear EST 23-
vc24h07.r1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone
IMAGE:775549 5' similar to SW:MRPI_HUMAN P33527 MULTIDRUG
RESISTANCE-ASSOCIATED PROTEIN 1. ;, mRNA sequence.
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                                                                                         Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                          EST
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4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                        house mouse
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="BACN37L08"
/note="end : SP6"
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11.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cgtcttcatggtccccctggagatgttggccct 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTGCCACCCGAATCATGGCCAGCAACCAGGAGATGCTACGGCACAAGGATGCACGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGCATGGCTTCCTGGCCTGGCCTGGTCTTGGCGCCTGCTGGTACCTGTCAACAAAGT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 591)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
                                                                                                                                                                                                                               BI960325 591 bp mrNA linear EST 22-OCT-200 HVSMEn0024D19f Hordeum vulgare rachis EST library HVcDNA0015 (normal) Hordeum vulgare cDNA clone HVSMEn0024D19f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wusrr.euu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                         BI960325.1 GI:16311580
                                                                                                                            Hordeum vulgare
                                                                                                                                             parley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 452
Location/Qualifiers
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314 286 1810
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150 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'. The CDNAS were ligated to LL-Sal38: 5'
GCTATTGACGTCGACTATCC 3' and LL-Sal38: 5'
GGATAGTCGACGTCAAT 3'. The CDNAS were size-selected and
amplified by long-range PCR using Ex Tag polymerase for 18
cycles. The PCR-amplifiable cDNA mixture went through
one round of equalization and was digested with Sal7NotI
and cloned into the Sal1/NotI sites of the pSPORTI
plasmid vector (Life Technologies). The library was
constructed by Dr. Minoru S. H. Ko and Dr. Xiaohong
Wang."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="embryo"
/dev_stage="11.5dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:775549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="
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Pred. No. 4.6;
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Best Local :
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ggggaaaagggtgatgcccaacaccaagaccgtggccgttgacctgggcctcatcctggt
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                                                         CGGCGGCCTCCTCGGCTACGACACCCCTCTGGAACGGCTCCGTCGTCGTCCCCCGCCGA
                                                                                                            caaggcctaccaggaccacggaatccgccccaccctggacgtgctggtcctctgggctca
                                                                                                                                                                                                                                                                                                                                                                                                         GTGCATCGAGAAGGCCGGCGTGGCGCACAAGATCGACTTCCGCGAGGGCCCCGGCGCTCCC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop:
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Total hd bases = 530
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: Permence stop: 592.
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100 Jordan Hall, C
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Fax: 864 656 4293
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,J., Oates,R. and Main,D.
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; plants were grown at Washington State University,
pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
lab at the University of California, Riverside total RNA
was prepared, poly(A) was purified, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 1211 c 128 g 113 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           above. For more details on library preparation and
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/lab_host="TJC121"
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/clone="HVSMEn0024D19f"
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Pred. No. 5
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Best Local S
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                                                                                                                                                                                                                                                                                Local Similarity
ACGTGCGCCGAGGACAGCGTCGCCATCAACACGGAGTCGGCCGTCAGGGTCAAGTCCG
                    aaaccgtcaacggggagcgccggggccatcggcaccctttgggccgtccggctgaggccag 568
                                                                                        tccacgcctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcacc
                                                                                                                            ACGAGTACGGCATCAGGTTCAACATGCCGAGCCAGCACATCGTCATCCGGAGGCTGACCT
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                                                               GCGTCTCCCCCACGAGCGCCATGATCGCGCTGGGCAGCGAGATGTCCGGCGGCATCCGCG
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945017C08.X1 945 - Mixed
(SK) Zea mays cDNA, mRNA
AW927362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanford University
855 California Ave, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 650 723 2227 Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University
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945017 row: C colu
                                                                                                                                                                                                                                                                                                                                                      /note="Organ: tassel, kernal, silk, husk, root, leaf;
/ector: pGAD10; Site_1: ECORI; cDNA library from fully
differentiated maize tissues from an active mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."

a 174 c 151 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/cultivar="W23"
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cggcgtgctctccttcaactgggtcaaggcctaccaggaccacggaatccgcccaccct 695
                                               CTGCGTCAAGTCCGGCGCCTCCAAGGTGGCCGTCAACGACGTCGTCTTCAAGAACATCCA
                                                                    caggeteaceetggaegaetaeatetaeceetggaggaacetegeeetagaeatggeeaa 635
                                                                                                                                         caacggggagcgccggggcatcggcaccctttgggccgtccggctgaggccagggaaagc 575
                                                                                                                                                                            ctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcaccaaaccgt 515
                                                                                                                                                                                                                                                                      catggtccccctggagatgttggccctcaacctgggggtcacccggcagaccgtccacgc 455
                                                                                                              CACCATGGACAACGTCTCCTACCCCATCATCATAGACCAGAAGTACTGCCCCAACAACAT 232
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1 (bases 1 to 534)
                                                                                                                                                                                                                                                                                                           Similarity 45...71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 707033 row: D col
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AW331023.1
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707033D10.x3 707 - Mixed adult tissues
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/vector: pGAD10; Site_1: EcoR1; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4/2/1/1/1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned."

186 c 131 g 89 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="707 - Mixe
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="tassel,
/dev_stage="adult"
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                                                                                195
                                                                                                                      389
                                        449
                                                                                                                                                              135 AGATCGAGGACTGCTACATCGTCTCCGGCGACGACTGCGTGGCCCGTGAAGAGCGGGTGGG 194
                                                                                                                                                                                                      329
                           tccacgcctggaagaaggtccttgagaaaaagggcctggtggccaccgacgtccttcacc 508
                                                                                                     tcgtcttcatggtccccctggagatgttggccctcaacctgggggtcacccggcagaccg 448
                                                                                                                                                                                     agattgcccgctccaccatcccctacggcaaccgggagctctggaggaaggtggggacgg 388
                                                                              ACGAGTACGGCATCAGGTTCAACATGCCGAGCCAGCACATCGTCATCCGGAGGCTGACCT 254
GCGTCTCCCCCACGAGCGCCATGATCGCGCTGGGCAGCGAGATGTCCGGCGGCATCCGCG 314
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Zea mays
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548 bp mRNA linear EST 30-MAY-2000 945017C08.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.
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1 (bases 1 to 548)
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Plate: 945017 row: C colu
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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Contact: Walbot V
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Maize ESTs from various cDNA libraries sequenced at Stanford University
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nilarity 48.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     108
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/ector: pGAD10; Site_1: EcoRI; cDNA library from fully 
differentiated malze tissues from an active Mutator plant. 
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, 
root, leaf). Unidirectionally cloned. New library number 
given to library 707 for additional sequencing." 
a 184 c 162 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="zea mays"
/cultivar="#23"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
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/dev_stage="fully-grown"
/lab_host="DH10B"
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Pred. No. 5.7;
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